1636
Box Seq

NEB-181

PATENT

Attorney's Docket No. _____

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: R. Vaisvila, et al.

#6a
3eta
4-5-02

| | |
|---|---|
| Application No.: 09/689,343 | Group No.: |
| Filed: October 12, 2000 | Examiner: |
| For: Method for Cloning And Producing The MseI Restriction Endonuclease | |

Box Sequence
Assistant Commissioner for Patents
Washington, D.C. 20231

## SUBMISSION OF "SEQUENCE LISTING," COMPUTER READABLE COPY, AND/OR AMENDMENT PERTAINING THERETO FOR BIOTECHNOLOGY INVENTION CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE

*(check and complete this item, if applicable)*

1. ☒ This replies to the Office Letter dated March 19, 2002 .

*NOTE: If these papers are filed before the office letter issues, adequate identification of the original papers should be made, e.g., in addition to the name of the inventor and title of invention, the filing date based on the "Express Mail" procedure, the application number from the return post card or the attorney's docket number added.*

☒ A copy of the Office Letter is enclosed.

### CERTIFICATION UNDER 37 C.F.R. §§ 1.8(a) and 1.10*
*(When using Express Mail, the Express Mail label number is mandatory; Express Mail certification is optional.)*

I hereby certify that, on the date shown below, this correspondence is being:

**MAILING**

☒ deposited with the United States Postal Service in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231

| 37 C.F.R. § 1.8(a) | 37 C.F.R. § 1.10* |
|---|---|
| ☒ with sufficient postage as first class mail. | ☐ as "Express Mail Post Office to Addressee" |
| | Mailing Label No. _____ (mandatory) |

**TRANSMISSION**

☐ transmitted by facsimile to the Patent and Trademark Office.

Date: 3 26 02

Signature

Melissa A. Jackson
*(type or print name of person certifying)*

*WARNING: Each paper or fee filed by Express Mail must have the number of the "Express Mail" mailing label placed thereon prior to mailing. 37 C.F.R. § 1.10(b).*
*"Since the filing of correspondence under § 1.10 without the Express Mail mailing label thereon. is an oversight that can be avoided by the exercise of reasonable care, requests for waiver of this requirement will not be granted on petition." Notice of Oct. 24, 1996, 60 Fed. Reg. 56,439, at 56,442.*

(Submission—Nucleotide and/or Amino Acid Sequence [9-37]—page 1 of 6).

## IDENTIFICATION OF PERSON MAKING STATEMENT

2.  I, __Gregory D. Williams__

*(type or print name of declarant signing below)*

state the following:

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APR 0 5 2002

TECH CENTER 1600/2900

## ITEMS BEING SUBMITTED

3.  Submitted herewith is/are:

*(check each item as applicable)*

A.  ☐ "Sequence Listing(s)" for the nucleotide and/or amino acid sequence(s) in this application. Each "Sequence Listing" is assigned a separate identifier as required in 37 C.F.R. § 1.821(c) and 37 C.F.R. §§ 1.822 and 1.823.

B.  ☐ An amendment to the description and/or claims, wherein reference is made to the sequence by use of the assigned identifier, as required in 37 C.F.R. § 1.821(d).

C.  ☒ A copy of each "Sequence Listing" submitted for this application in computer readable form, in accordance with the requirements of 37 C.F.R. §§ 1.821(e) and 1.824.

D.  ☐ Please transfer to this application, in accordance with 37 C.F.R. § 1.821(e), the computer readable copy(ies) from applicant's other application identified as follows:

In re application of:

Application No.:  0  /       Group No.:

Filed:       Examiner:

For:

The Computer readable form(s) of applicant's other application corresponds to the "Sequence indentifier(s)" of the application as follows:

Computer Readable Form      "Sequence Identifier"

(other application)      (this application)

E. ☒ A statement that the content of each "Sequence Listing" submitted and each computer readable copy are the same, as required in 37 C.F.R. § 1.821(g).

    ☐ Because the statement is not made by a person registered to practice before the Office, the statement is verified as required in 37 C.F.R. § 1.821(b).

F. ☒ Because this submission is made in fulfilling the requirement under 37 C.F.R. § 1.821(g), a statement that the submission includes no new matter.

    ☐ Because the statement is not made by a person registered to practice before the Office, the statement is verified, as required in 37 C.F.R. § 1.821(g).

## STATEMENT THAT "SEQUENCE LISTING" AND COMPUTER READABLE COPY ARE THE SAME AND/OR THAT PAPERS SUBMITTED INCLUDES NO NEW MATTER

4. I hereby state:

*(complete applicable item A and/or B)*

A. ☒ Each computer readable form submitted in this application, including those forms requested to be transferred from applicant's other application, is the same as the "Sequence Listing" to which it is indicated to relate.

B. ☒ All papers accompanying this submission, or for which a request for transfer from applicants' other application, introduce no new matter.

## STATUS

5. Applicant is

☒ a small entity. A statement:

    ☐ is attached.

    ☒ was already filed.

☐ other than a small entity.

# EXTENSION OF TERM

6.

NOTE: *"Extension of Time in Patent Cases (Supplement Amendments)—If a timely and complete response has been filed after a Non-Final Office Action, an extension of time is not required to permit filing and/or entry of an additional amendment after expiration of the shortened statutory period.*

*If a timely response has been filed after a Final Office Action, an extension of time is required to permit filing and/or entry of a Notice of Appeal or filing and/or entry of an additional amendment after expiration of the shortened statutory period unless the timely-filed response placed the application in condition for allowance. Of course, if a Notice of Appeal has been filed within the shortened statutory period, the period has ceased to run." Notice of Dec. 10, 1985 (1061 O.G. 34-35).*

NOTE: See 37 C.F.R. § 1.645 for extensions of time in interference proceedings and 37 C.F.R. § 1.550(c) for extensions of time in reexamination proceedings.

7.    The proceedings herein are for a patent application and the provisions of 37 C.F.R. § 1.136 apply.

*(complete (a) or (b) as applicable)*

(a)  ☐  Applicant petitions for an extension of time under 37 C.F.R. § 1.136 (fees: 37 C.F.R. § 1.17(a)(1)-(4)) for the total number of months checked below:

| Extension (months) | Fee for other than small entity | Fee for small entity |
|---|---|---|
| ☐ one month | $ 110.00 | $ 55.00 |
| ☐ two months | $ 390.00 | $ 195.00 |
| ☐ three months | $ 890.00 | $ 445.00 |
| ☐ four months | $ 1,390.00 | $ 695.00 |

Fee:    $_____

If an additional extension of time is required, please consider this a petition therefor.

*(check and complete the next item, if applicable)*

☐  An extension for _____ months has already been secured. The fee paid therefor of $_____ is deducted from the total fee due for the total months of extension now requested.

Extension fee due with this request    $_____

## OR

(b)  ☒  Applicant believes that no extension of term is required. However, this conditional petition is being made to provide for the possibility that applicant has inadvertently overlooked the need for a petition for extension of time.

(Submission—Nucleotide and/or Amino Acid Sequence [9-37]—page 4 of 6)

## FEE PAYMENT

8. ☐ Attached is a ☐ check ☐ money order in the amount of $ _____

    ☐ Authorization is hereby made to charge the amount of $ _____

    ☐ to Deposit Account No. _____

    ☐ to Credit card as shown on the attached credit card information authorization form PTO-2038.

*WARNING: Credit card information should not be included on this form as it may become public.*

☐ Charge any additional fees required by this paper or credit any overpayment in the manner authorized above.

A duplicate of this paper is attached.

## FEE DEFICIENCY

9.

*NOTE: If there is a fee deficiency and there is no authorization to charge an account, additional fees are necessary to cover the additional time consumed in making up the original deficiency. If the maximum, six-month period has expired before the deficiency is noted and corrected, the application is held abandoned. In those instances where authorization to charge is included, processing delays are encountered in returning the papers to the PTO Finance Branch in order to apply these charges prior to action on the cases. Authorization to charge the deposit account for any fee deficiency should be checked. See the Notice of April 7, 1986, 1065 O.G. 31-33.*

10. ☒ If any additional extension and/or fee is required, charge

    ☒ Deposit Account No. ___14-0740___

    ☐ Credit card as shown on the attached credit card information authorization form PTO-2038.

*WARNING: Credit card information should not be included on this form as it may become public.*

## SIGNATURE(s)

Gregory D. Williams
_____
(type or print name of person signing statement)

_____
Signature

3/25/07
_____
Date
32 Tozer Road
Beverly, MA   01915
_____
P.O. Address of Signatory

*(if applicable)*
Telephone No. (978 ) 927-5054 X:292
Reg. No. 30901
Customer No.:   28986

☐ Inventor(s)
☐ Assignee of complete interest
☐ Person authorized to sign on behalf of assignee
☒ Practitioner of record
☐ Filed under Rule 34(a)
☐ Registration No. _____
☐ Other _____
    *(specify identity of declarant)*

*(complete the following, if applicable)*

New England Biolabs, Inc.

*(type name of assignee)*
32 Tozer Road, Beverly, MA  01915

Address of assignee

---

Secretary

Title of person authorized to sign on behalf of
assignee

A "STATEMENT UNDER 37 C.F.R. § 3.73(b)" is attached.

Assignment recorded in PTO on _____

Reel _____ Frame _____

## RECEIVED

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## TECH CENTER 1600/2900

Reg. No.: 30901

Tel. No.: ( 978 ) 927-5054 X:292

Customer No.: 28986

SIGNATURE OF PRACTITIONER
Gregory D. Williams
General Counsel
*(type or print name of practitioner)*
New England Biolabs, Inc.
32 Tozer Road
P.O. Address

Beverly, MA  01915

UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231
www.uspto.gov

| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. | CONFIRMATION NO. |
|---|---|---|---|---|
| 09/689,343 | 10/12/2000 | Romualdas Vaisvila | NEB-181 | 7976 |

28986        7590        03/19/2002

NEW ENGLAND BIOLABS, INC.
32 TOZER ROAD
BEVERLY, MA   01915

| EXAMINER |
|---|
| GUZO, DAVID |

| ART UNIT | PAPER NUMBER |
|---|---|
| 1636 | |

DATE MAILED: 03/19/2002

5

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TECH CENTER 1600/2900

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 07-01)

**UNITED STATES DEPARTMENT OF COMMERCE**
**Patent and Trademark Office**

Address: ASSISTANT COMMISSIONER FOR PATENTS
Washington, D.C. 20231

| APPLICATION NO./ CONTROL NO. | FILING DATE | FIRST NAMED INVENTOR / PATENT IN REEXAMINATION | ATTORNEY DOCKET NO. |
|---|---|---|---|

| EXAMINER |
|---|

## RECEIVED

APR 0 5 2002

| ART UNIT | PAPER |
|---|---|
| | 5 |

TECH CENTER 1600/2900

DATE MAILED:

**Please find below and/or attached an Office communication concerning this application or proceeding.**

Commissioner of Patents and Trademarks

—SEE ATTACHMENT—

## Attachment

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth below or on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures and on the attached Raw Sequence Listing Error Report.

Applicant is given ONE MONTH, or THIRTY DAYS, whichever is longer, from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to David Guzo whose telephone number is (703) 308-1906. The examiner can normally be reached on Monday-Thursday from 8:00 AM to 5:30 PM. The examiner can also be reached on alternate Fridays.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Irem Yucel, can be reached on (703) 305-1998. The fax phone number for the organization where this application or proceeding is assigned is (703) 308-4242.

Any inquiry of a general nature or relating to the status of this application or proceeding or relating to attachments to this Office Action should be directed to Patent Analyst Zeta Adams whose telephone number is (703) 305-3291.

David Guzo
March 18, 2002

DAVID GUZO
PRIMARY EXAMINER
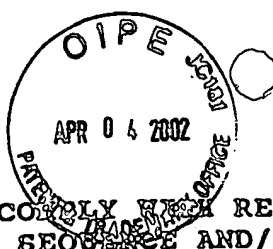
*Applicants' Copy*

Application No. 09/689343

# NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

☑ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure, a paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

☑ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☐ 7.

Other: _____

Applicant must provide:

☑ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

☑ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

☑ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
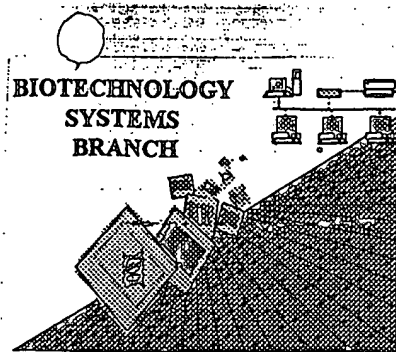For PatentIn software help, call (703) 557-0400

BIOTECHNOLOGY
SYSTEMS
BRANCH

# RAW SEQUENCE LISTING
# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/689,343_

Source: _OIPE_

Date Processed by STIC: _10/27/2000_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.


FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:


## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

**APR 0 4 2002** OIPE — PATENT TRADEMARK OFFICE

<u>ERROR DETECTED</u>   SUGGESTED  CORRECTION      SERIAL NUMBER: _09/689,343_

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

TECH CENTER 1600/2900   RECEIVED APR 30 2002

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 ✓ _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _4_____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ _____ Use of n's or Xaa's (NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)   Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)   Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/689,343

DATE: 10/27/2000
TIME: 08:36:04

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Output Set: N:\CRF3\10272000\I689343.raw

```
  3 <110> APPLICANT: VAISVILA, ROMUALDAS
  4         MORGAN, RICHARD D.
  5         KUCERA, REBECCA B.
  6         CLAUS, TOBY E.
  7         RALEIGH, ELISABETH A.
  9 <120> TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE MseI RESTRICTION
 10       ENDONUCLEASE
 12 <130> FILE REFERENCE: NEB-181
 14 <140> CURRENT APPLICATION NUMBER: US/09/689,343
 15 <141> CURRENT FILING DATE: 2000-10-12
 17 <160> NUMBER OF SEQ ID NOS: 9
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 903
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Micrococcus sp.
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)..(900)
 30 <400> SEQUENCE: 1
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 33  1               5                  10                  15
 35 gag gcg gac aac ctc gat ttc att caa acg ctc ccc gac gcg agc ttc      96
 36 Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe
 37                 20                  25                  30
 39 cga atg atc tac atc gat ccg ccg ttc aac aca ggg cga acg cag cgg     144
 40 Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
 41             35                  40                  45
 43 ctt cag tcg ctc aag acg acc cgc tcg gtc aca ggg tcg cga gtc ggc     192
 44 Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
 45         50                  55                  60
 47 ttc aaa ggc cag acg tac gac acg gtc aag agc act ctg cac tcg tat     240
 48 Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
 49  65                  70                  75                  80
 51 gac gac gct ttc acc gac tat tgg tcg ttc ctc gaa ccg cgt ctc ctg     288
 52 Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
 53                 85                  90                  95
 55 gag gct tgg cgg ttg ctc acc cct gac ggc gcg ctc tat ctt cat ctg     336
 56 Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
 57             100                 105                 110
 59 gat tac cgc gag gtt cac tac gcc aag gtc gtc ctc gac gcg atg ttc     384
 60 Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
 61             115                 120                 125
 63 gga cgc gaa agc ttc ctg aac gag ctg atc tgg gcg tac gac tac ggc     432
 64 Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
 65         130                 135                 140
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                        PATENT APPLICATION: US/09/689,343 TIME: 08:36:04

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   69 145             150             155                 160
   71 tat gtg aag gac ccg aac aac tac gtc tgg aac ggt cag gat gta gat   528
   72 Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
   73                 165             170                 175
   75 cgc gag ccc tac atg gcg ccc ggg ctc gtt aca ccc gag aag gta gcg   576
   76 Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
   77                 180             185             190
   79 ctt ggc aag ctg ccc acc gac gtc tgg tgg cac aca atc gtt ccg cct   624
   80 Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
   81         195             200             205
   83 gcg agc aaa gag cgc acc ggg tac gcg aca cag aag ccg gtc ggc atc   672
   84 Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
   85         210             215                 220
   87 atc cgt cgc atg att cag gcg agc agc aat gaa ggc gac tgg gtt ctg   720
   88 Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
   89 225             230             235                 240
   91 gat ttc ttc gct ggt agt ggg acg acc ggc gcc gcg gcc cgc cag ctc   768
   92 Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
   93                 245             250             255
   95 gga cgc cgt ttt gtg ctc gta gac gtc aac cca gaa gca atc gcg gta   816
   96 Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
   97             260             265             270
   99 atg gca aaa cgg ttg gat gac ggg gca ttg gac acc agc gtg acg atc   864
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  104 Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly
  105         290             295             300
  108 <210> SEQ ID NO: 2
  109 <211> LENGTH: 300
  110 <212> TYPE: PRT
  111 <213> ORGANISM: Micrococcus sp.
  113 <400> SEQUENCE: 2
  114 Met Pro Ile Ser Thr Val Trp Thr Pro Asp Gly Asp Asp Leu Ile Val
  115  1               5               10                  15
  117 Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe
  118             20              25              30
  120 Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
  121         35              40              45
  123 Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
  124     50              55              60
  126 Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
  127 65              70              75                  80
  129 Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
  130                 85              90              95
  132 Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
  133             100             105             110
```

RAW SEQUENCE LISTING           DATE: 10/27/2000
PATENT APPLICATION: US/09/689,343     TIME: 08:36:04

Input Set : A:\Neb-181.app
Output Set: N:\CRF3\l0272000\I689343.raw

```
135 Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
136         115                 120                 125
138 Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
139         130  .               135                 140
141 Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
142 145                 150                 155                 160
144 Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
145             165                 170                 175
147 Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
148             180                 185                 190
150 Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
151         195                 200                 205
153 Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
154         210                 215                 220
156 Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
157 225                 230                 235                 240
159 Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
160              245                 250                     255
162 Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
163         260                 265                 270
165 Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
166         275                 280                 285
168 Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly
169         290                 295                 300
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 1236
174 <212> TYPE: DNA
175 <213> ORGANISM: Unknown
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Unknown Organism: ENVIRONMENTAL DNA
180 <220> FEATURE:
181 <221> NAME/KEY: CDS
182 <222> LOCATION: (1)..(1233)
184 <400> SEQUENCE: 3
185 atg cct aca ctg gat tgg ccc ggt aaa cag tta agc ttc cca cca gct   48
186 Met Pro Thr Leu Asp Trp Pro Gly Lys Gln Leu Ser Phe Pro Pro Ala
187  1               5                  10                  15
189 acc tcc ttg cat ctg gag agt gtg gtc act gag gga gcg gag tca ccg   96
190 Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro
191             20                  25                  30
193 cct aat cgt ctg att tgg gcg gac aac ctg ccg cta atg gta gat ttg  144
194 Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu
195         35                  40                  45
197 ttg gcc gaa tat gaa ggg aaa atc gat ctg atc tac gcc gat ccc cct  192
198 Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro
199         50                  55                  60
201 ttt ttt acg gat cgt act tat gcg gcg cga att ggt cat ggg gag gat  240
202 Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
203 65                  70                  75                  80
```

```
205 tcg cgt cgt cca caa acc tgg cag ctt gca gaa gga tat acg gac gag   288
206 Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
207                 85              90                  95
209 tgg aag gat tta gat gaa tac ctg gac ttc ctt tat cca cgc ctg gta   336
210 Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
211             100             105                 110
213 ctg atg tat cga ctg ctg gca cca cac gga acg ctc tac ttg cac ctg   384
214 Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
215         115             120                 125
217 gac tgg cac gcc aat gcc tac gta cgt gta ctg ctt gat gag atc ttc   432
218 Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
219         130             135             140
221 ggg cga cag cgg ttt ctc aac gag atc gtc tgg atc tat cac ggc ccc   480
222 Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
223 145             150                 155                 160
225 tca gcc atc cga cgc gcc ttc aag cgc aaa cat gat acc atc ttg gtt   528
226 Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
227                 165                 170                 175
229 tat gtg aaa ggt gaa aac tat aca ttc aat gcg gat gcg gtt cgt caa   576
230 Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln
231             180             185                 190
W--> 233 cct tac cat ccg agc acq cat aag acc ttc gct tcc tcc ccg aag gcc   624
W--> 234 Pro Tyr His Pro Ser Xad His Lys Thr Phe Ala Ser Ser Pro Lys Ala
235             195             200                 205
237 ggc ttt ggt aag gtg ccg gat ctg cag cgc ggc aaa gtg ccc gaa gac   672
238 Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp
239 210             215                 220
241 tgg tgg tat ttt ccg gtc gtg gcc cgt cta cac cga gaa cgg agc ggc   720
242 Trp Trp Tyr Phe Pro Val Val Ala Arg Leu His Arg Glu Arg Ser Gly
243 225             230             235                 240
245 tat ccg act caa aag cct caa gcc ttg ctg gag cgg atc ctg ctg gcc   768
246 Tyr Pro Thr Gln Lys Pro Gln Ala Leu Leu Glu Arg Ile Leu Leu Ala
247             245                 250                 255
249 tcc tcg aac gca ggc gat ctg gtg gca gac ttc ttc tgc ggc tca ggg   816
250 Ser Ser Asn Ala Gly Asp Leu Val Ala Asp Phe Phe Cys Gly Ser Gly
251             260             265                 270
253 aca acc gct gtg gtg gca gcc cgt ctg gga cgg cgc ttc ctg gtc aac   864
254 Thr Thr Ala Val Val Ala Ala Arg Leu Gly Arg Arg Phe Leu Val Asn
255         275             280                 285
257 gat gca agc tgg cgc gcc gtt cat gtg aca cgc aca cgc ttg cta cgc   912
258 Asp Ala Ser Trp Arg Ala Val His Val Thr Arg Thr Arg Leu Leu Arg
259     290             295                 300
261 gag gga gta agt ttc act ttt gaa cgc cag gaa act ttt act cta cct   960
262 Glu Gly Val Ser Phe Thr Phe Glu Arg Gln Glu Thr Phe Thr Leu Pro
263 305             310             315                 320
265 atc cag cca ctt cca cca gat tgg ttg atc atc gcc gag gag cag att   1008
266 Ile Gln Pro Leu Pro Pro Asp Trp Leu Ile Ile Ala Glu Glu Gln Ile
267             325             330                 335
269 cgc ctc caa gca ccc ttt ctc gta gat ttt tgg gaa gtg gac gat caa   1056
```

→ see item 10 on Err Summary Sheet

```
270 Arg Leu Gln Ala Pro Phe Leu Val Asp Phe Trp Glu Val Asp Asp Gln
271             340                 345                 350
273 tgg gat ggc aaa atc ttc cgc agc cgt cat caa ggc tta cgc tcc cgc    1104
274 Trp Asp Gly Lys Ile Phe Arg Ser Arg His Gln Gly Leu Arg Ser Arg
275             355                 360                 365
277 ctt cag gag cag gcg ccg ctc tct cta cca ttg acc ggg aat gga ctg    1152
278 Leu Gln Glu Gln Ala Pro Leu Ser Leu Pro Leu Thr Gly Asn Gly Leu
279             370                 375                 380
281 ttg tgt gta cgg gta gtg agc cgt gaa ggg gaa tac tat gag ttc aca    1200
282 Leu Cys Val Arg Val Val Ser Arg Glu Gly Glu Tyr Tyr Glu Phe Thr
283 385                 390                 395                 400
285 ggt cga gcc gat agc cct cac ccc gta tcg ttt tga                    1236
286 Gly Arg Ala Asp Ser Pro His Pro Val Ser Phe
287                 405                 410
290 <210> SEQ ID NO: 4
291 <211> LENGTH: 411
292 <212> TYPE: PRT
293 <213> ORGANISM: Unknown
W--> 295 <220> FEATURE:
W--> 295 <223> OTHER INFORMATION:
295 <400> SEQUENCE: 4
296 Met Pro Thr Leu Asp Trp Pro Gly Lys Gln Leu Ser Phe Pro Pro Ala
297  1               5                  10                  15
299 Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro
300             20                  25                  30
302 Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu
303             35                  40                  45
305 Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro
306             50                  55                  60
308 Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
309 65                  70                  75                  80
311 Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
312                 85                  90                  95
314 Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
315             100                 105                 110
317 Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
318             115                 120                 125
320 Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
321 130                 135                 140
323 Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
324 145                 150                 155                 160
326 Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
327                 165                 170                 175
329 Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln
330             180                 185                 190
W--> 332 Pro Tyr His Pro Ser Xaa His Lys Thr Phe Ala Ser Ser Pro Lys Ala
333             195                 200                 205
335 Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp
336 210                 215                 220
```

*→ see item 7 on Erra Summary Sheet*

*→ see item 10 on Erra Summary Sheet*

VERIFICATION SUMMARY                          DATE: 10/27/2000
PATENT APPLICATION:  US/09/689,343           TIME: 08:36:05

Input Set : A:\Neb-181.app
Output Set: N:\CRF3\10272000\I689343.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:295 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:295 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:332 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:332 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:332 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:474 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:474 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: